



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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171003

STIC-Biotech/ChemLib

From: Hines, Ja-Na
Sent: Tuesday, November 08, 2005 2:38 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search

Good Afternoon,
I would like to request a sequence and interference search
for application 10/043,344. In particular SEQ ID NO:50, 61, 74 and 85.

Thanks so much!!
Ja-Na Hines (76048)
AU:1645
Office: Rem 3B29
Mailbox: Rem 3C18
x20859

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 11/9/05
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# 4
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: [Signature]
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2005, 19:01:45 ; Search time 28.9506 Seconds
(without alignments)
116.322 Million cell updates/sec

Title: US-10-043-344-61
Perfect score: 186
Sequence: 1 FTSGTLEGGFYGPGEGLGKFLAHDKKVLGVFS 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	92.5	648	2 S70907	transferrin-bindin
2	159	85.5	625	2 D64107	transferrin-bindin
3	159	85.5	630	2 S70909	transferrin-bindin
4	159	85.5	631	2 S70910	transferrin-bindin
5	157	84.4	654	2 S70905	transferrin-bindin
6	156	83.9	631	2 S70908	transferrin-bindin
7	150	80.6	660	2 S70904	transferrin-bindin
8	113.5	61.0	599	2 JN0818	transferrin-bindin
9	109	58.6	547	2 S49814	transferrin-bindin
10	107	57.5	547	2 S49815	transferrin-bindin
11	107	57.5	547	2 A44796	transferrin-bindin
12	102	54.8	593	2 S27483	transferrin-bindin
13	102	54.8	593	2 B44796	transferrin-bindin
14	97	52.2	737	2 H81070	lactoferrin-bindin
15	97	52.2	741	2 D81798	lactoferrin-bindin
16	94.5	50.8	711	2 S70660	transferrin-bindin
17	91.5	49.2	711	2 JN0820	transferrin-bindin
18	91.5	49.2	712	2 E81196	transferrin-bindin
19	90.5	48.7	689	2 S70661	transferrin-bindin
20	90.5	48.7	698	2 D81832	transferrin-bindin
21	78	41.9	289	2 G64105	transferrin-bindin
22	66	35.5	488	2 E81003	transferrin-bindin
23	66	35.5	497	2 C82025	probable periplasm
24	60	32.3	742	2 A49341	isocitrate dehydro
25	59.5	32.0	389	2 T44975	conserved hypotet
26	59	31.7	241	2 AG2915	hypothetical prote
27	59	31.7	241	2 B37690	hypothetical prote
28	56	30.1	394	2 A86431	outer membrane lip
29	55	29.6	200	2 AH3260	

30	54.5	29.3	193	2 H83794	hypothetical prote
31	54.5	29.3	367	2 AF1537	B. subtilis YxjH a
32	54	29.0	1035	2 AD3203	autotransporter pr
33	53.5	28.8	312	2 T37150	probable oxidoredu
34	53.5	28.8	337	2 A69355	adenylosuccinate s
35	53	28.5	265	2 H97349	alpha/beta superfa
36	52.5	28.2	506	1 S34286	pisatin demethylas
37	52.5	28.2	515	1 S45583	pisatin demethylas
38	52.5	28.2	1171	2 T42372	probable guanilate
39	52.5	28.2	1256	2 J80209	brain-specific ang
40	51.5	27.7	367	2 AE1180	B. subtilis YxjH a
41	51.5	27.7	499	2 D72342	tldD protein - The
42	51.5	27.7	707	1 S69781	outer membrane pro
43	51	27.4	148	2 C65088	hypothetical prote
44	51	27.4	163	2 C91092	hypothetical prote
45	51	27.4	163	2 G85937	hypothetical prote

ALIGNMENTS

RESULT 1

S70907
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB12)
C:Species: Haemophilus influenzae
A:Variety: strain SB12
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S70907; S73320
R:Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.
Mol. Microbiol. 19, 575-586, 1996
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A:Reference number: S70901; MUID:96228706; PMID:8830248
A:Accession: S70907
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-648 <LOQ>
A:Cross-references: UNIPROT:Q48040; EMBL:U15054
A:Experimental source: strain SB12, clone DS-1047-1-2
R:Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A:Reference number: S73320
A:Accession: S73320
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-533, 'V', 535-542, 'I', 544-559, 'G', 561-648 <LOW>
A:Cross-references: EMBL:U15054; NID:g1223946; PIDN:AAC43930.1; PID:g1223947
A:Experimental source: strain SB12, clone DS-1047-1-2
C:Genetics:
A:Gene: tbp2
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-648/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 92.5%; Score 172; DB 2; Length 648;
Best Local Similarity 94.3%; Pred. No. 2.1e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTSGTLEGGFYGPGEGLGKFLAHDKKVLGVFS 35
|||||
Db 291 FTSGTLEGGFYGPGEGLGKFLAGDKKVLGVFS 325
|||||

RESULT 2

D64107
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: D64107
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 456-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: D64107
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-625 <TIGR>
A;Cross-references: UNIPROT:P44971; GB:U32780; GB:L42023; NID:g1574020; PIDN:AAC22657.1;
C;Genetics:
C;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-625/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 85.5%; Score 159; DB 2; Length 625;
Best Local Similarity 85.7%; Pred. No. 1.2e-13;
Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FTSEGTLEGGFYGPGEGLGKFLAHDKKVLGVFS 35
||| ||||| : ||||| |||||
DB 287 FTREGTLEGGFYGNGBELGGKFLAGDKKVLGVFS 321

RESULT 3

S70309
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB30)
C;Species: Haemophilus influenzae
A;Variety: strain SB30
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70309; S73322
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.H.
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A;Reference number: S70301; MUID:96228706; PMID:8830248
A;Accession: S70309
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-630 <LOO>
A;Cross-references: UNIPROT:Q48042; EMBL:U15056
A;Experimental source: strain SB30, clone DS-1047-3-3
R;Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A;Reference number: S73320
A;Accession: S73322
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448, 'T', 450, 'I', 452-630 <LOW>
A;Cross-references: EMBL:U15056; NID:g1223950; PIDN:AAC43932.1; PID:g1223951
A;Experimental source: strain SB30, clone DS-1047-3-3
C;Genetics:
C;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-630/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 85.5%; Score 159; DB 2; Length 630;
Best Local Similarity 85.7%; Pred. No. 1.2e-13;
Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FTSEGTLEGGFYGPGEGLGKFLAHDKKVLGVFS 35
||| ||||| : ||||| |||||
DB 290 FTSEGTLEGGFYGNGBELGGKFLASDKKVLGVFS 324

RESULT 4

S70310
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB32)
C;Species: Haemophilus influenzae
A;Variety: strain SB32
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70310; S73323
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.H.
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes

C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor

Qy 7 LEGGYPGEQELGGKFLAHDKKVLGVFS 35
 |||||: |::| :::: | |||:
Db 326 LEGGFFGDNGEELAGRFISNDNSVFGVFA 354

Search completed: November 9, 2005, 19:24:01
Job time : 34.9506 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:42:14 ; Search time 125.914 Seconds
(without alignments)
126.074 Million cell updates/sec

Title: US-10-043-344-50

Perfect score: 164

Sequence: 1 LEGFYGPKEBELGFRFLAGDKVGVFSK 31

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	89.6	625	1 TBP2_HAEIN	P44971 haemophilus
2	145	88.4	648	2 Q48040	Q48040 haemophilus
3	139	84.8	631	2 Q48041	Q48041 haemophilus
4	135	82.3	630	2 Q48042	Q48042 haemophilus
5	135	82.3	631	2 Q48043	Q48043 haemophilus
6	131	79.9	644	2 Q48034	Q48034 haemophilus
7	131	79.9	654	2 Q48038	Q48038 haemophilus
8	127	77.4	566	2 Q6H804	Q6H804 neisseria m
9	127	77.4	582	2 Q9FC53	Q9FC53 neisseria m
10	127	77.4	593	2 Q6H8W5	Q6H8W5 neisseria c
11	127	77.4	593	2 Q6H8W6	Q6H8W6 neisseria c
12	127	77.4	594	2 Q6H8W3	Q6H8W3 neisseria f
13	127	77.4	602	2 Q53991	Q53991 neisseria m
14	125	76.2	594	2 Q6H8W0	Q6H8W0 neisseria f
15	125	76.2	594	2 Q6H8W1	Q6H8W1 neisseria f
16	125	76.2	660	2 Q57443	Q57443 haemophilus
17	124	75.6	702	2 Q85050	Q85050 moraxella c
18	123	75.0	593	2 Q6H8V1	Q6H8V1 neisseria g
19	123	75.0	593	2 Q6H8W4	Q6H8W4 neisseria f
20	123	75.0	594	2 Q6H8V8	Q6H8V8 neisseria m
21	123	75.0	711	2 Q92FD4	Q92FD4 moraxella c
22	123	75.0	712	2 Q92106	Q92106 moraxella c
23	123	75.0	713	2 Q85051	Q85051 moraxella c
24	123	75.0	714	2 Q85056	Q85056 moraxella c
25	119	72.6	681	2 Q9EXC7	Q9EXC7 neisseria m
26	119	72.6	688	2 Q86397	Q86397 neisseria m
27	119	72.6	693	2 Q51285	Q51285 neisseria m
28	119	72.6	693	2 Q9JPL8	Q9JPL8 neisseria m
29	119	72.6	695	2 Q9FCR8	Q9FCR8 neisseria m
30	119	72.6	696	2 Q9EXA7	Q9EXA7 neisseria m
31	119	72.6	696	2 Q9RLM1	Q9RLM1 neisseria m

32	119	72.6	698	2 Q9JPL7	Q9JPL7 neisseria m
33	119	72.6	699	2 Q9EXC4	Q9EXC4 neisseria m
34	119	72.6	711	2 Q51284	Q51284 neisseria m
35	119	72.6	714	2 Q6H8T4	Q6H8T4 neisseria p
36	119	72.6	714	2 Q6H8T5	Q6H8T5 neisseria p
37	119	72.6	715	2 Q9AKU6	Q9AKU6 neisseria m
38	117	71.3	697	2 Q9EXC8	Q9EXC8 neisseria m
39	116	70.7	680	2 Q53990	Q53990 neisseria m
40	116	70.7	705	2 Q51286	Q51286 neisseria m
41	115	70.1	547	2 Q44124	Q44124 actinobacil
42	115	70.1	547	2 Q44168	Q44168 actinobacil
43	115	70.1	547	2 Q44170	Q44170 actinobacil
44	115	70.1	669	2 Q9FCR5	Q9FCR5 neisseria m
45	115	70.1	669	2 Q9FC50	Q9FC50 neisseria m

ALIGNMENTS

RESULT 1

ID	TBP2_HAEIN	STANDARD;	PRT;	625 AA.
AC	P44971;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Probable transferrin-binding protein 2 precursor.			
GN	Name=tbpB; Synonyms=tbp2; OrderedLocusNames=HI0995;			
OS	Haemophilus influenzae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Haemophilus.			
OX	NCBI_TaxID=727;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Rd / KW20 / ATCC 51907;			
RX	MEDLINE=95350630; PubMed=7542800;			
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,			
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,			
RA	McKenny K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,			
RA	Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,			
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,			
RA	Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,			
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,			
RA	Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,			
RA	Venter J.C.;			
RT	"Whole-genome random sequencing and assembly of Haemophilus influenzae			
RL	Rd.;"			
CC	Science 269:496-512(1995).			
CC	-1- FUNCTION: Acts as a transferrin receptor and is required for			
CC	transferrin utilization (by similarity).			
CC	-1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid			
CC	anchor (Probable).			

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CC	EMBL; U32780; AAC22657.1; -.
CC	PIR; D64107; D64107.
DR	TIGR; HI0995; -.
DR	InterPro; IPR001677; Transferrin_bind.
DR	Pfam; PF01298; Lipoprotein_5; 1.
DR	PROSITE; PS00013; PROXAR_LIPOPROTEIN; 1.
KW	Complete proteome; Lipoprotein; Outer membrane; Palmitate; Receptor; Signal.
FT	SIGNAL
FT	CHAIN
FT	LIPID
FT	LIPID
FT	Potential.
FT	Probable transferrin-binding protein 2.
FT	N-palmitoyl cysteine (Probable).
FT	S-diacylglycerol cysteine (Probable).

	PIR; S70908;	S70908.
DR	GO:	GO:0016020; C:membrane; IEA.
DR	GO:	GO:0004998; F:transferrin receptor activity; IEA.
DR	InterPro:	IPR001677; Transferrin_bind.
DR	Pfam:	PF01298; Lipoprotein 5; 1
DR	SEQUENCE	631 AA; 69770 MW; 8C607778953F3B39 CRC64;
 Query Match 84.8%; Score 139; DB 2; Length 631; Best Local Similarity 83.9%; Pred.No. 1.7e-10; Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		
Oy	1	LEGGFYGPKGEELGFRLAGDKKVGVSFAK 31 : :
Dd	296	LEGFGYPNGEELGGKFAGDNRVGVFSAK 326 : :
 RESULT 4		
Q48042	PRELIMINARY;	PRT; 630 AA.
ID Q48042	AC Q48042;	
DT 01-NOV-1996	(TrEMBLrel. 01,	Created)
DT 01-NOV-1996	(TrEMBLrel. 01,	Last sequence update)
DT 01-MAR-2004	(TrEMBLrel. 26,	Last annotation update)
DE	Transferrin binding protein 2.	
GN	Name=cbp2;	
OS	Haemophilus influenzae.	
OC	Bacteria; Proteobacteria;	Gammaproteobacteria; Pasteurellales;
OX	Pasteurellaceae; Haemophilus.	
NCBI_TaxID=727;	[1]	
RN	SEQUENCE FROM N.A.	
RP	STRAIN=SB30;	
RC	MEDLINE=96228706; PubMed=8830248;	
RA	Loosmore S.M., Yang Y.P.; Coleman D.C., Shortreed J.M., England D.M., Harkness R.E., Pele S.C., Klein M.H.; "Cloning and expression of the Haemophilus influenzae transferrin receptor genes." Mol. Microbiol. 19:575-586(1996).	
RL	EMBL; U15056; AAC43932.1; -.	
RR	PIR; S70909; S70909.	
DR	GO:	GO:0016020; C:membrane; IEA.
DR	GO:	GO:0004998; F:transferrin receptor activity; IEA.
DR	InterPro:	IPR001677; Transferrin_bind.
DR	Pfam:	PF01298; Lipoprotein 5; 1.
DR	SEQUENCE	630 AA; 69573 MW; 6FCB2D1B6B642CB4 CRC64;
 Query Match 82.3%; Score 135; DB 2; Length 630; Best Local Similarity 83.9%; Pred.No. 6e-10; Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;		
Oy	1	LEGGFYGPKGEELGFRLAGDKKVGVSFAK 31 : :
Dd	296	LEGFGYPAEELGGKFADNRVGVFSAK 326 : :
 RESULT 5		
Q48043	PRELIMINARY;	PRT; 631 AA.
ID Q48043	AC Q48043;	
DT 01-NOV-1996	(TrEMBLrel. 01,	Created)
DT 01-NOV-1996	(TrEMBLrel. 01,	Last sequence update)
DT 01-MAR-2004	(TrEMBLrel. 26,	Last annotation update)
DE	Transferrin binding protein 2.	
GN	Name=cbp2;	
OS	Haemophilus influenzae.	
OC	Bacteria; Proteobacteria;	Gammaproteobacteria; Pasteurellales;
OX	Pasteurellaceae; Haemophilus.	
NCBI_TaxID=727;	[1]	
RN	SEQUENCE FROM N.A.	
RP	STRAIN=SB32;	
RC	MEDLINE=96228706; PubMed=8830248;	
RA	Loosmore S.M., Yang Y.P.; Coleman D.C., Shortreed J.M., England D.M.,	

```

RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RL receptor genes.";
RL Mol. Microbiol. 19:575-586(1996).
DR EMBL; U15057; AAC43933.1; -.
DR PIR; S70910; S70910.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 631 AA; 70104 MW; E43FF90516F4EDC9 CRC64;

Query Match 82.3%; Score 135; DB 2; Length 631;
Best Local Similarity 83.9%; Pred. No. 6e-10;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :||| :|||
Db 296 LEGGYGNABELGGKFLASDKKVGVSFAK 326

RESULT 6
Q48034
ID Q48034 PRELIMINARY; PRT; 644 AA.
AC Q48034;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DL63;
RX MEDLINE=95197237; PubMed=7890373;
RA Gray-Owen S.D., Loosmore S., Schryvers A.B.;
RT "Identification and characterization of genes encoding the human
RT transferrin-binding proteins from Haemophilus influenzae.";
RL Infect. Immun. 63:1201-1210(1995).
DR EMBL; U10882; AAA80491.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 644 AA; 70797 MW; 613F9627D8422616 CRC64;

Query Match 79.9%; Score 131; DB 2; Length 644;
Best Local Similarity 80.6%; Pred. No. 2.2e-09;
Matches 25; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :||| :|||
Db 294 LEGGYGEGELGGKFLAHDKKVLGVFSFAK 324

RESULT 7
Q48038
ID Q48038 PRELIMINARY; PRT; 654 AA.
AC Q48038;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=PAK 12085;
RX MEDLINE=96228706; PubMed=8830248;
RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.";
RL Mol. Microbiol. 19:575-586(1996).
DR EMBL; U15053; AAC43928.1; -.
DR PIR; S70905; S70905.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 654 AA; 71834 MW; FF3EC728BE5F05A6 CRC64;

Query Match 79.9%; Score 131; DB 2; Length 654;
Best Local Similarity 80.6%; Pred. No. 2.2e-09;
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :||| :|||
Db 296 LEGGYGNABELGGKFLANDERKVGVSFAK 326

RESULT 8
Q6H8U4
ID Q6H8U4 PRELIMINARY; PRT; 566 AA.
AC Q6H8U4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Transferrin binding protein B (fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha261;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704752; CAG28834.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT NON_TER 566
SQ SEQUENCE 566 AA; 61751 MW; B0FCA99B682412D8 CRC64;

Query Match 77.4%; Score 127; DB 2; Length 566;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGRFLAGDKKVGVSFAK 31
||||| :||| :||| :||| :||| :|||
Db 291 LEGGYGPGDELGGKFLANDKKVLAVFSFAK 321

RESULT 9
Q9FCS3
ID Q9FCS3 PRELIMINARY; PRT; 582 AA.
AC Q9FCS3;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Transferrin binding protein B (fragment).
GN Name=tbpB;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2717;
RX MEDLINE=20407297; PubMed=10948108;
RA DOI=10.1128/JAI.68.9.4938-4947.2000;
RA Rokbi B., Renaud-Mongenie G., Mignon M., Danve B., Poncet D.,
RA Chabanel C., Caugant D.A., Quentin-Millet M.J.;
RT "Allelic diversity of the two transferrin binding protein B gene
RT isotypes among a collection of Neisseria meningitidis strains
RT representative of serogroup B disease: implication for the composition
RT of a recombinant TbpB-based vaccine.";
RL Infect. Immun. 68:4938-4947(2000).
DR EMBL; AJ279554; CAC05588.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
DR FT CHAIN 1
DR NON_TER 1
DR SQ SEQUENCE 582 AA; 63426 MW; 26A94AD04F2507F4 CRC64;

Query Match 77.4%; Score 127; DB 2; Length 582;
Best Local Similarity 77.4%; Pred. No. 7e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEELGFRFLAGDKKVGVSFAK 31
Db 307 LEGGYGPGQDELGGKFLANDKKVLAVFSK 337

RESULT 10
Q6H8W5
ID Q6H8W5 PRELIMINARY; PRT; 593 AA.
AC Q6H8W5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria cinerea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=483;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=415;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704731; CAG28813.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
DR SQ SEQUENCE 593 AA; 64218 MW; 8F67EALB15A9FEA9 CRC64;

Query Match 77.4%; Score 127; DB 2; Length 593;
Best Local Similarity 77.4%; Pred. No. 7.1e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEELGFRFLAGDKKVGVSFAK 31
Db 318 LEGGYGPGQDELGGKFLANDKKVLAVFSK 348

RESULT 11
Q6H8W6
ID Q6H8W6 PRELIMINARY; PRT; 593 AA.
AC Q6H8W6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]

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OS Neisseria sicca.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=490;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9913;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704730; CAG28812.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
DR SQ SEQUENCE 593 AA; 64257 MW; 46187C48497275BA CRC64;

Query Match 77.4%; Score 127; DB 2; Length 593;
Best Local Similarity 77.4%; Pred. No. 7.1e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEELGFRFLAGDKKVGVSFAK 31
Db 318 LEGGYGPGQDELGGKFLANDKKVLAVFSK 348

RESULT 12
Q6H8W3
ID Q6H8W3 PRELIMINARY; PRT; 594 AA.
AC Q6H8W3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria flavescens.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=484;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13120;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704733; CAG28815.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
DR SQ SEQUENCE 594 AA; 64390 MW; F096DB9B9046D0B CRC64;

Query Match 77.4%; Score 127; DB 2; Length 594;
Best Local Similarity 77.4%; Pred. No. 7.1e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEELGFRFLAGDKKVGVSFAK 31
Db 318 LEGGYGPGQDELGGKFLANDKKVLAVFSK 348

RESULT 13
Q53991
ID Q53991 PRELIMINARY; PRT; 602 AA.
AC Q53991
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE TbpB precursor.
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=2713;
RX MEDLINE=98148004; PubMed=9479046; DOI=10.1016/S0378-1119(97)00646-X;
RA Legrain M., Rokbi B., Villevall D., Jacobs E.;
RT "Characterization of Genetic exchanges between various highly
RT divergent tbpBs, having occurred in Neisseria meningitidis.";
RL Gene 208:51-59(1998).
DR EMBL; AJ223044; CAA1047.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 602 AA; 65488 MW; 74641BF77B61C257 CRC64;

Query Match 77.4%; Score 127; DB 2; Length 602;
Best Local Similarity 77.4%; Pred. No. 7.2e-09;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LEGGFGPKGBELGFRFLAGDKKVGVSFAK 31
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DB 327 LEGGFGPQGDELGGKFLANDKKVLAVFSK 357

RESULT 14
Q6H8W0 PRELIMINARY; PRT; 594 AA.
AC Q6H8W0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria flavescens.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=484;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=414, and 3191;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704736; CAG28818.2; -.
DR EMBL; AJ704734; CAG28816.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 594 AA; 64345 MW; 6200B465E793F20A CRC64;

Query Match 76.2%; Score 125; DB 2; Length 594;
Best Local Similarity 77.4%; Pred. No. 1.3e-08;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LEGGFGPKGBELGFRFLAGDKKVGVSFAK 31
| | | | | | | | | | | | | | | | | | | | | |
DB 318 LEGGFGPQGDELGGKFLAKDKVLAVFSK 348

RESULT 15
Q6H8W1 PRELIMINARY; PRT; 594 AA.
AC Q6H8W1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria flavescens.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.

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OX NCBI_TaxID=484;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3656;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704735; CAG28817.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 594 AA; 64331 MW; 7663C043033D615B CRC64;

Query Match 76.2%; Score 125; DB 2; Length 594;
Best Local Similarity 77.4%; Pred. No. 1.3e-08;
Matches 24; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LEGGFGPKGBELGFRFLAGDKKVGVSFAK 31
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DB 318 LEGGFGPQGDELGGKFLAKDKVLAVFSK 348

Search completed: November 9, 2005, 19:16:34
Job time : 134.914 secs

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Result No.	Score	Query			DB	ID	Description
		Match	Length	†			
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2	145	88.4	648	2	S70907	transferrin-binding	
3	139	84.8	631	2	S70908	transferrin-binding	
4	135	82.3	630	2	S70909	transferrin-binding	
5	135	82.3	631	2	S70910	transferrin-binding	
6	131	79.9	654	2	S70905	transferrin-binding	
7	125	76.2	660	2	S70904	transferrin-binding	
8	119	72.6	711	2	S70660	transferrin-binding	
9	115	70.1	547	2	S49815	transferrin-binding	
10	115	70.1	547	2	A44796	transferrin-binding	
11	115	70.1	689	2	S70661	transferrin-binding	
12	115	70.1	689	2	D81832	transferrin-binding	
13	114	69.5	599	2	JN0818	transferrin-binding	
14	111	67.7	711	2	JN0820	transferrin-binding	
15	111	67.7	712	2	E81196	transferrin-binding	
16	105	64.0	547	2	S49814	transferrin-binding	
17	104	63.4	737	2	H81070	lactoferrin-binding	
18	104	63.4	741	2	D81798	lactoferrin-binding	
19	102	62.2	593	2	S27483	transferrin-binding	
20	102	62.2	593	2	B44796	transferrin-binding	
21	66	40.2	488	2	E81003	transferrin-binding	
22	66	40.2	497	2	C82025	probable periplasm	
23	62	37.8	289	2	G43105	transferrin-binding	
24	59	36.0	595	2	A83020	probable carbamoyl	
25	57	34.8	742	2	A49341	isocitrate dehydro	
26	54	32.9	389	2	T44975	dehydrogenase [imp	
27	52.5	32.0	521	2	T27606	hypothetical prote	
28	52	31.7	316	2	T19435	hypothetical prote	
29	52	31.7	539	2	T28770	hypothetical prote	

A;Reference number: S73320
A;Accession: S73320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-533,'V',535-542,'I',544-559,'G',561-648 <LOW>
A;Cross-references: EMBL:U15054; NID:gl223946; PIDN:AAC43930.1; PID:gl223947
A;Experimental source: strain SB12, clone DS-1047-1-2
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-648/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 88.4%; Score 145; DB 2; Length 648;
Best Local Similarity 87.1%; Pred. No. 2.2e-12;
Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEGGYGKGEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 297 LEGGYGEGELGKFLAGDKKVGVSFAK 327

RESULT 3
S70908
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C;Species: Haemophilus influenzae
A;Variety: strain SB29
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70908; S73321
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A;Reference number: S70901; MUID:96228706; PMID:8830248
A;Accession: S70908
A;Molecule type: DNA
A;Residues: 1-631 <LOO>
A;Cross-references: UNIPROT:Q48041; EMBL:U15055
A;Experimental source: strain SB29, clone DS-1090-3-2
R;Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A;Reference number: S73320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-250,'L',252-349,'RTDATTN',357-631 <LOW>
A;Cross-references: EMBL:U15055; NID:gl223948; PIDN:AAC43931.1; PID:gl223949
A;Experimental source: strain SB29, clone DS-1090-3-2
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 84.8%; Score 139; DB 2; Length 631;
Best Local Similarity 83.9%; Pred. No. 1.5e-11;
Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGYGKGEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 296 LEGGYGNGELGKFLAGDNRVGVVSFAK 326

RESULT 4
S70909
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB30)
C;Species: Haemophilus influenzae
A;Variety: strain SB30
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70909; S73322
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A;Reference number: S70901; MUID:96228706; PMID:8830248

A;Accession: S70909
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-630 <LOO>
A;Cross-references: UNIPROT:Q48042; EMBL:U15056
A;Experimental source: strain SB30, clone DS-1047-3-3
R;Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A;Reference number: S73320
A;Accession: S73322
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448,'T',450,'I',452-630 <LOW>
A;Cross-references: EMBL:U15056; NID:gl223950; PIDN:AAC43932.1; PID:gl223951
A;Experimental source: strain SB30, clone DS-1047-3-3
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-630/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 82.3%; Score 135; DB 2; Length 630;
Best Local Similarity 83.9%; Pred. No. 5.5e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGKGEELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 296 LEGGYGPNAEELGKFLASDKKVGVSFAK 326

RESULT 5
S70910
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB32)
C;Species: Haemophilus influenzae
A;Variety: strain SB32
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70910; S73323
R;Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A;Reference number: S70901; MUID:96228706; PMID:8830248
A;Accession: S70910
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-631 <LOO>
A;Cross-references: UNIPROT:Q48043; EMBL:U15057
A;Experimental source: strain SB32, clone DS-1047-4-10
R;Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A;Reference number: S73320
A;Accession: S73323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-241,'P',243-420,'C',422-508,'A',510-631 <LOW>
A;Cross-references: EMBL:U15057; NID:gl223952; PIDN:AAC43933.1; PID:gl223953
A;Experimental source: strain SB32, clone DS-1047-4-10
C;Genetics:
A;Gene: tbp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 82.3%; Score 135; DB 2; Length 631;
Best Local Similarity 83.9%; Pred. No. 5.5e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGKGEELGFRFLAGDKKVGVSFAK 31
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Db 296 LEGGYGPNAEELGKFLASDKKVGVSFAK 326

RESULT 6
S70905

C;Accession: S70660
R;Legrain, M.; Findeli, A.; Villevall, D.; Quentin-Millet, M.J.; Jacobs, E.
Mol. Microbiol. 19, 159-169, 1996
A;Title: Molecular characterization of hybrid Tbp2 proteins from Neisseria meningitidis.
A;Reference number: S70659; MUID:96419172; PMID:8821945
A;Accession: S70660
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-711 <LEG>
A;Cross-references: UNIPROT:Q51284; EMBL:Z50731; NID:g1177568; PIDN:CAA90598.1; PID:g117
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-711/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match . 72.6%; Score 119; DB 2; Length 711;
Best Local Similarity 77.4%; Pred. No. 1.1e-08;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEGGFGPKGBELGFRFLAGDKKVFVFSAK 31
| | | | | | | | | | | | | | | | | | | |
Db 335 LSGGFFGPKGBELGFRFLSDKKVAVVSAS 365

RESULT 9
S49815
transferrin-binding protein - Actinobacillus pleuropneumoniae
C;Species: Actinobacillus pleuropneumoniae
C;Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S49815
R;Bunka, S.; Potter, A.; Gerlach, G.
submitted to the EMBL Data Library, November 1994
A;Description: Cloning and sequencing of the transferrin-binding protein genes of Actino
A;Reference number: S49814
A;Accession: S49815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <BUN>
A;Cross-references: UNIPROT:Q44168; EMBL:Z46775; NID:g577528; PIDN:CAA86730.1; PID:g5775
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

Query Match . 70.1%; Score 115; DB 2; Length 547;
Best Local Similarity 67.7%; Pred. No. 3.1e-08;
Matches 21; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LEGGFGPKGBELGFRFLAGDKKVFVFSAK 31
| | | | | | | | | | | | | | | | | | | |
Db 272 LGGFGPKAEEMAGKFVANDKSLFAVFSAS 302

RESULT 10
A44796
transferrin-binding protein, tfba - Actinobacillus pleuropneumoniae
C;Species: Actinobacillus pleuropneumoniae
C;Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44796; S27484
R;Gerlach, G.F.; Khashinsky, S.; Anderson, C.; Potter, A.A.; Willson, P.J.
Infect. Immun. 60, 3253-3261, 1992
A;Title: Characterization of two genes encoding distinct transferrin-binding proteins in
A;Reference number: A44796; MUID:92347999; PMID:1639494
A;Contents: AP205 serotype 7
A;Accession: A44796
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-547 <GER>
A;Cross-references: UNIPROT:Q44170; EMBL:M85275; NID:g141842; PIDN:AAA21929.1; PID:g1418
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:109735, NCBIP:109736)
C;Genetics:
A;Gene: tfba

F1-20/Domain: signal sequence #status predicted <SIG>
F121-711/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 67.7%; Score 111; DB 2; Length 711;
Best Local Similarity 71.0%; Pred. No. 1.5e-07;
Matches 22; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEGGFGPKGEBELGFRFLAGDKKVFVFSK 31
DB 335 LSGGFFPGQEBELGFRFLSDQKVAVGSK 365

RESULT 15

E81196
transferrin-binding protein 2 NMB0460 [imported] - Neisseria meningitidis (strain MC58 a
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: E81196
R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: E81196
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-712 <TET>
A:Cross-references: UNIPROT:Q9K0V0; GB:AE002402; GB:AE002098; NID:g7225683; PIDN:AAF4089
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0460
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

Query Match 67.7%; Score 111; DB 2; Length 712;
Best Local Similarity 71.0%; Pred. No. 1.5e-07;
Matches 22; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LEGGFGPKGEBELGFRFLAGDKKVFVFSK 31
DB 336 LSGGFFPGQEBELGFRFLSDQKVAVGSK 366

Search completed: November 9, 2005, 19:23:55
Job time : 26.642 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	164	100.0	31	14	US-10-043-344-50	Sequence 50, Appl
2	145	88.4	648	14	US-10-043-344-109	Sequence 109, App
3	139	84.8	631	14	US-10-043-344-111	Sequence 111, App
4	135	82.3	630	14	US-10-043-344-113	Sequence 113, App
5	135	82.3	631	14	US-10-043-344-115	Sequence 115, App
6	131	79.9	644	14	US-10-043-344-6	Sequence 6, Appl
7	131	79.9	654	14	US-10-043-344-12	Sequence 12, Appl
8	125	76.2	365	14	US-10-043-344-156	Sequence 156, App
9	125	76.2	404	14	US-10-043-344-155	Sequence 155, App
10	125	76.2	411	14	US-10-043-344-154	Sequence 154, App
11	125	76.2	417	14	US-10-043-344-153	Sequence 153, App

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RESULT 2
US-10-043-344-109
; Sequence 109, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-109

Query Match      88.4%; Score 145; DB 14; Length 648;
Best Local Similarity 87.1%; Pred. No. 1.1e-12;
Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 297 LEGGYGPEGLGKFLAGDKKVGVSFAK 327

RESULT 3
US-10-043-344-111
; Sequence 111, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-111

Query Match      84.8%; Score 139; DB 14; Length 631;
Best Local Similarity 83.9%; Pred. No. 8.3e-12;
Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 296 LEGGYGNGELGKFLAGDNRRVGVSFAK 326

RESULT 4
US-10-043-344-113
; Sequence 113, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-113

Query Match      82.3%; Score 135; DB 14; Length 630;
Best Local Similarity 83.9%; Pred. No. 3.3e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 296 LEGGYGNAELGGKFLASDKKVGVSFAK 326

RESULT 5
US-10-043-344-115
; Sequence 115, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-115

Query Match      82.3%; Score 135; DB 14; Length 631;
Best Local Similarity 83.9%; Pred. No. 3.3e-11;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 296 LEGGYGNAELGGKFLASDKKVGVSFAK 326

RESULT 6
US-10-043-344-6
; Sequence 6, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
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; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-6

Query Match 79.9%; Score 131; DB 14; Length 644;
Best Local Similarity 80.6%; Pred. No. 1.3e-10;
Matches 25; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Oy 1 LEGGYGPKBELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 294 LEGGYGPKBELGFRFLAGDKKVGVSFAK 324

RESULT 7
US-10-043-344-12
; Sequence 12, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-12

Query Match 79.9%; Score 131; DB 14; Length 654;
Best Local Similarity 80.6%; Pred. No. 1.3e-10;
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Oy 1 LEGGYGPKBELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 296 LEGGYGPKBELGFRFLAGDKKVGVSFAK 326

RESULT 8
US-10-043-344-156
; Sequence 156, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.

; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-156

Query Match 76.2%; Score 125; DB 14; Length 365;
Best Local Similarity 77.4%; Pred. No. 5.5e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Oy 1 LEGGYGPKBELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 294 LEGGYGPKBELGFRFLAGDKKVGVSFAK 324

RESULT 9
US-10-043-344-155
; Sequence 155, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-155

Query Match 76.2%; Score 125; DB 14; Length 404;
Best Local Similarity 77.4%; Pred. No. 6.2e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Oy 1 LEGGYGPKBELGFRFLAGDKKVGVSFAK 31
|||||:||||:||||:||||:|||||
Db 294 LEGGYGPKBELGFRFLAGDKKVGVSFAK 324

RESULT 10
US-10-043-344-154
; Sequence 154, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Murdin, Andrew D.

```
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-154

Query Match          76.2%; Score 125; DB 14; Length 411;
Best Local Similarity 77.4%; Pred. No. 6.3e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEELGFRFLAGDKKVGVSFAK 31
||||||| ||||| :||| :|||||
Db 294 LEGGYGPNABELGGKFLATDNRVGVFSK 324

RESULT 11
US-10-043-344-153
; Sequence 153, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Mordin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-153

Query Match          76.2%; Score 125; DB 14; Length 417;
Best Local Similarity 77.4%; Pred. No. 6.4e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEELGFRFLAGDKKVGVSFAK 31
||||||| ||||| :||| :|||||
Db 294 LEGGYGPNABELGGKFLATDNRVGVFSK 324

RESULT 12
US-10-043-344-152
; Sequence 152, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Mordin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 152
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-152

Query Match          76.2%; Score 125; DB 14; Length 430;
Best Local Similarity 77.4%; Pred. No. 6.6e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEELGFRFLAGDKKVGVSFAK 31
||||||| ||||| :||| :|||||
Db 294 LEGGYGPNABELGGKFLATDNRVGVFSK 324

RESULT 13
US-10-043-344-151
; Sequence 151, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Mordin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 151
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-151

Query Match          76.2%; Score 125; DB 14; Length 463;
Best Local Similarity 77.4%; Pred. No. 7.2e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGYGPKGEELGFRFLAGDKKVGVSFAK 31
||||||| ||||| :||| :|||||
Db 294 LEGGYGPNABELGGKFLATDNRVGVFSK 324

RESULT 14
US-10-043-344-150
; Sequence 150, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Mordin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
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; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-150

Query Match 76.2%; Score 125; DB 14; Length 529;
Best Local Similarity 77.4%; Pred. NO. 8.3e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGYPGKGEELGFRFLAGDKKVFVFSK 31
| | | | | : | | | | | : | | | | |
Db 294 LEGGYPGNAEELGGKFLATDNRVFGVFSK 324

RESULT 15

US-10-043-344-149
; Sequence 149, Application US/10043344
; Publication No. US2003008086A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Mordin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043.344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-043-344-149

Query Match 76.2%; Score 125; DB 14; Length 547;
Best Local Similarity 77.4%; Pred. NO. 8.6e-10;
Matches 24; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LEGGYPGKGEELGFRFLAGDKKVFVFSK 31
| | | | | : | | | | | : | | | | |
Db 294 LEGGYPGNAEELGGKFLATDNRVFGVFSK 324

Search completed: November 9, 2005, 19:10:50
Job time : 133.802 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:42:14 ; Search time 142.16 Seconds
(without alignments)
126.074 Million cell updates/sec

Title: US-10-043-344-61

Perfect score: 186

Sequence: 1 FTSGTLEGGYFGPEGQELGKFLAHDKKVLGVFS 35

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	100.0	644	Q48034	haemophilus
2	172	92.5	648	Q48040	haemophilus
3	159	85.5	625	1 TBP2	HAETIN
4	159	85.5	630	Q48042	haemophilus
5	159	85.5	631	Q48043	haemophilus
6	157	84.4	654	Q48038	haemophilus
7	156	83.9	631	Q48041	haemophilus
8	150	80.6	660	Q57443	haemophilus
9	136.5	73.4	566	Q6H804	neisseria m
10	136.5	73.4	582	Q9FC83	neisseria m
11	136.5	73.4	593	Q6H8W5	neisseria c
12	136.5	73.4	593	Q6H8W6	neisseria s
13	136.5	73.4	594	Q6H8W3	neisseria f
14	136.5	73.4	602	Q53991	neisseria m
15	134.5	72.3	594	Q6H8W0	neisseria f
16	134.5	72.3	594	Q6H8W1	neisseria f
17	132.5	71.2	593	Q6H8V1	neisseria s
18	132.5	71.2	593	Q6H8W4	neisseria f
19	132.5	71.2	594	Q6H8V8	neisseria m
20	124	66.7	713	Q85051	moraxella c
21	121	65.1	702	Q85050	moraxella c
22	118	63.4	711	Q92F04	moraxella c
23	118	63.4	712	Q92I06	moraxella c
24	118	63.4	714	Q85056	moraxella c
25	115	61.8	706	Q85052	moraxella c
26	115	61.8	709	Q85055	moraxella c
27	114.5	61.6	571	Q6H8U1	neisseria m
28	113.5	61.0	410	Q6H8U3	neisseria m
29	113.5	61.0	567	Q6H8U0	neisseria m
30	113.5	61.0	569	Q6H8T9	neisseria m
31	113.5	61.0	569	Q6H8U2	neisseria m

32	113.5	61.0	570	2	Q6H8U7	Q6H8U7 neisseria m
33	113.5	61.0	572	2	Q6H8U6	Q6H8U6 neisseria m
34	113.5	61.0	573	2	Q6H8T6	Q6H8T6 neisseria m
35	113.5	61.0	579	2	Q6H8T7	Q6H8T7 neisseria m
36	113.5	61.0	579	2	Q9FC81	Q9FC81 neisseria m
37	113.5	61.0	586	2	Q9RDV1	Q9RDV1 neisseria m
38	113.5	61.0	599	1	TBB2_NEIMB	Q05988 neisseria m
39	113.5	61.0	599	2	Q6H8V0	Q6H8V0 neisseria l
40	113.5	61.0	599	2	Q6H8V2	Q6H8V2 neisseria p
41	113.5	61.0	599	2	Q6H8V4	Q6H8V4 neisseria p
42	113.5	61.0	599	2	Q6H8V5	Q6H8V5 neisseria p
43	113.5	61.0	599	2	Q6H8V9	Q6H8V9 neisseria l
44	113.5	61.0	599	2	Q71US2	Q71US2 neisseria m
45	113.5	61.0	605	2	Q6H8V3	Q6H8V3 neisseria p

ALIGNMENTS

RESULT 1
Q48034 ID Q48034 PRELIMINARY; PRT; 644 AA.
AC Q48034; TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbpB;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellales; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DL63;
RX MEDLINE=95197237; PubMed=7890373;
RA Gray-Owen S.D., Loosmore S., Schryvers A.B.;
RT "Identification and characterization of genes encoding the human
transferrin-binding proteins from Haemophilus influenzae.";
RL Infect. Immun. 63:1201-1210(1995).
DR EMBL; U10882; AAA80491.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein 5; 1.
SQ SEQUENCE 644 AA; 70797 MW; 613F9627D8422616 CRC64;
Query Match 100.0%; Score 186; DB 2; Length 644;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTSGTLEGGYFGPEGQELGKFLAHDKKVLGVFS 35
|||||
Db 288 FTSGTLEGGYFGPEGQELGKFLAHDKKVLGVFS 322
RESULT 2
Q48040 ID Q48040 PRELIMINARY; PRT; 648 AA.
AC Q48040;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellales; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB12;
RX MEDLINE=96228706; PubMed=8830248;

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RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.", 19:575-586(1996).
RL Mol. Microbiol. 19:575-586(1996).
DR EMBL; U15054; AAC43930.1; -.
DR PIR; S70907;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 648 AA; 71246 MW; D89690AE33891A5A CRC64;

Query Match 92.5%; Score 172; DB 2; Length 648;
Best Local Similarity 94.3%; Pred. No. 9.7e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGGKFLAHDKKVLGVFS 35
Db 291 FTSEGTLEGGFYGPGEQELGGKFLAGDKKLVGVFS 325

RESULT 3
TBP2 HAEIN STANDARD; PRT; 625 AA.
ID TBP2 HAEIN STANDARD; PRT; 625 AA.
AC P44971;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable transferrin-binding protein 2 precursor.
GN Name=tbp2; Synonyms=tbp2; OrderedLocusNames=HI0995;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.P.,
RA Karlayev A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.A., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: Acts as a transferrin receptor and is required for
CC transferrin utilization (by similarity).
CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC anchor (Probable).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; U32780; AAC22657.1; -.
DR PIR; D64107; D64107.
DR TIGR; HI0995; -.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome; Lipoprotein; Outer membrane; Palmitate; Receptor;
KW Signal.
FT SIGNAL 1 17 Potential.

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FT CHAIN 18 625 Probable transferrin-binding protein 2.
FT LIPID 18 18 N-palmitoyl cysteine (Probable).
FT LIPID 18 18 S-diacylglycerol cysteine (Probable).
SQ SEQUENCE 625 AA; 69031 MW; 52EPEC97B5ED4E9A CRC64;

Query Match 85.5%; Score 159; DB 1; Length 625;
Best Local Similarity 85.7%; Pred. No. 5.6e-13;
Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGGKFLAHDKKVLGVFS 35
Db 287 FTREGTLEGGFYGPNGEELGGKFLAGDKKLVGVFS 321

RESULT 4
Q48042 PRELIMINARY; PRT; 630 AA.
ID Q48042 PRELIMINARY; PRT; 630 AA.
AC Q48042;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB30;
RX MEDLINE=96228706; PubMed=8830248;
RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.";
RL Mol. Microbiol. 19:575-586(1996).
DR EMBL; U15056; AAC43932.1; -.
DR PIR; S70909; S70909.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 630 AA; 69573 MW; 6FCB2D1B6B642C84 CRC64;

Query Match 85.5%; Score 159; DB 2; Length 630;
Best Local Similarity 85.7%; Pred. No. 5.6e-13;
Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGGKFLAHDKKVLGVFS 35
Db 290 FTSEGTLEGGFYGPNAEELGGKFLASDKKLVGVFS 324

RESULT 5
Q48043 PRELIMINARY; PRT; 631 AA.
ID Q48043 PRELIMINARY; PRT; 631 AA.
AC Q48043;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SB32;
RX MEDLINE=96228706; PubMed=8830248;
RA Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin

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RT receptor genes";
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15057; AAC43933.1; -.
DR PIR; S70910; S70910.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 631 AA; 70104 MW; B43FF90516F4EDC9 CRC64;

Query Match      85.5%; Score 159; DB 2; Length 631;
Best Local Similarity 85.7%; Pred. No. 5,6e-13;
Matches 30; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGKFLAHDKKVLGVFS 35
Db 290 FTSEGTLEGGFYGPGEQELGKFLASDKKVLGVFS 324

RESULT 6
Q48038 PRELIMINARY; PRT; 654 AA.
AC Q48038;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=cbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAK 12085;
RX MEDLINE=96228706; PubMed=8830248;
RA Loomore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.";
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15053; AAC43928.1; -.
DR PIR; S70905; S70905.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 654 AA; 71834 MW; PF3EC728BE5F05A6 CRC64;

Query Match      84.4%; Score 157; DB 2; Length 654;
Best Local Similarity 82.9%; Pred. No. 1.1e-12;
Matches 29; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGKFLAHDKKVLGVFS 35
Db 290 FTSEGTLEGGFYGPGEQELGKFLANDEKVLGVFS 324

RESULT 7
Q48041 PRELIMINARY; PRT; 631 AA.
AC Q48041;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=cbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=SB29;
RX MEDLINE=96228706; PubMed=8830248;
RA Loomore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.";
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15055; AAC43931.1; -.
DR PIR; S70908; S70908.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 631 AA; 69770 MW; 8C607778953F3B39 CRC64;

Query Match      83.9%; Score 156; DB 2; Length 631;
Best Local Similarity 82.9%; Pred. No. 1.5e-12;
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGKFLAHDKKVLGVFS 35
Db 290 FTSEGTLEGGFYGPGEQELGKFLAGDNRVGVFS 324

RESULT 8
Q57443 PRELIMINARY; PRT; 660 AA.
AC Q57443;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein 2.
GN Name=cbp2;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Minna, and Egan;
RX MEDLINE=96228706; PubMed=8830248;
RA Loomore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
RA Harkness R.E., Pele S.C., Klein M.H.;
RT "Cloning and expression of the Haemophilus influenzae transferrin
RT receptor genes.";
RL Mol. Microbiol. 19:575-586 (1996).
DR EMBL; U15052; AAC43926.1; -.
DR EMBL; U15051; AAC43924.1; -.
DR PIR; S70904; S70904.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 660 AA; 73069 MW; 87E32401D6BDEP26 CRC64;

Query Match      80.6%; Score 150; DB 2; Length 660;
Best Local Similarity 80.8%; Pred. No. 1e-11;
Matches 28; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FTSEGTLEGGFYGPGEQELGKFLAHDKKVLGVFS 35
Db 288 FTSEGTLEGGFYGPGEQELGKFLATDNRVGVFS 322

RESULT 9
Q6H8U4 PRELIMINARY; PRT; 566 AA.
ID Q6H8U4
AC Q6H8U4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=cbpB;
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OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha261;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704752; CAG28834.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT NON_TER 566
SQ SEQUENCE 566 AA; 61751 MW; 80FCA99B682412D8 CRC64;

Query Match 73.4%; Score 136.5; DB 2; Length 566;
Best Local Similarity 75.0%; Pred. No. 6e-10;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 FTSEG-TLEGGFYGPQGLGGKFLAHDKKVLGVFS 35
Db 284 FVSDSDSLEGGFYGPQGLGGKFLANDKKVLAVFS 319

RESULT 10
Q9FCS3
ID Q9FCS3 PRELIMINARY; PRT; 582 AA.
AC Q9FCS3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Namestbpb;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2717;
RX MEDLINE=20407297; PubMed=10948108;
RX DOI=10.1128/IAI.68.9.4938-4947.2000;
RA Rokbi B., Renauld-Wongene G., Mignon M., Danve B., Poncet D.,
RA Chabanel C., Caugant D.A., Quentin-Willet M.J.;
RT Allelic diversity of the two transferrin binding protein B gene
RT isotypes among a collection of Neisseria meningitidis strains
RT representative of serogroup B disease: implication for the composition
RT of a recombinant TbpB-based vaccine.;
RL Infect. Immun. 68:4938-4947(2000).
DR EMBL; AJ279554; CAC05588.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT CHAIN <1 582 transferrin binding protein B.
SQ SEQUENCE 582 AA; 63426 MW; 26A94AD04F2507F4 CRC64;

Query Match 73.4%; Score 136.5; DB 2; Length 582;
Best Local Similarity 75.0%; Pred. No. 6.2e-10;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 FTSEG-TLEGGFYGPQGLGGKFLAHDKKVLGVFS 35
Db 300 FVSDSDSLEGGFYGPQGLGGKFLANDKKVLAVFS 335

RESULT 11
Q6H8W5
ID Q6H8W5 PRELIMINARY; PRT; 593 AA.

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AC Q6H8W5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Namestbpb;
OS Neisseria cinerea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=483;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=415;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704731; CAG28813.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 593 AA; 64218 MW; 8F67EA1B15A9FEA9 CRC64;

Query Match 73.4%; Score 136.5; DB 2; Length 593;
Best Local Similarity 75.0%; Pred. No. 6.3e-10;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 FTSEG-TLEGGFYGPQGLGGKFLAHDKKVLGVFS 35
Db 311 FVSDSDSLEGGFYGPQGLGGKFLANDKKVLAVFS 346

RESULT 12
Q6H8W6
ID Q6H8W6 PRELIMINARY; PRT; 593 AA.
AC Q6H8W6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Namestbpb;
OS Neisseria sicca.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=490;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9913;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704730; CAG28812.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
SQ SEQUENCE 593 AA; 64257 MW; 46187C48497275BA CRC64;

Query Match 73.4%; Score 136.5; DB 2; Length 593;
Best Local Similarity 75.0%; Pred. No. 6.3e-10;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 FTSEG-TLEGGFYGPQGLGGKFLAHDKKVLGVFS 35
Db 311 FVSDSDSLEGGFYGPQGLGGKFLANDKKVLAVFS 346

RESULT 13
Q6H8W3
ID Q6H8W3 PRELIMINARY; PRT; 594 AA.
AC Q6H8W3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.

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DE Transferrin binding protein B.
GN Name=tbpB;
OS Neisseria flavescens.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=484;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=414, and 3191;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704736; CAG28818.2; -.
DR EMBL; AJ704734; CAG28816.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein 5; 1.
SQ SEQUENCE 594 AA; 64345 MW; 6200E45E793F20A CRC64;

Query Match 72.3%; Score 134.5; DB 2; Length 594;
Best Local Similarity 75.0%; Pred. No. 1.2e-09;
Matches 27; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 FTSEG-TLEGGFVGPGEQELGGKFLAHDKKVLGVFS 35
Db |||:|||||||:||||||| ||| |||
311 FVSDSDSLEGGFYGPQDELGGKFLARKKKVLAVFS 346

Search completed: November 9, 2005, 19:16:34
Job time : 142.16 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:42:14 ; Search time 32.4938 Seconds
(without alignments)
126.074 Million cell updates/sec

Title: US-10-043-344-74

Perfect score: 47

Sequence: 1 LEGGFYGP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	60	Q6DKQ8	Q6dkq8 neisseria m
2	47	100.0	410	Q6H8U3	Q6h8u3 neisseria m
3	47	100.0	526	Q71R42	Q71r42 haemophilus
4	47	100.0	545	Q71R38	Q71r38 haemophilus
5	47	100.0	547	Q44124	Q44124 actinobacil
6	47	100.0	547	Q44168	Q44168 actinobacil
7	47	100.0	547	Q44170	Q44170 actinobacil
8	47	100.0	560	Q71R40	Q71r40 haemophilus
9	47	100.0	566	Q6H8U4	Q6h8u4 neisseria m
10	47	100.0	567	Q6H8U0	Q6h8u0 neisseria m
11	47	100.0	569	Q6H8T9	Q6h8t9 neisseria m
12	47	100.0	569	Q6H8U2	Q6h8u2 neisseria m
13	47	100.0	570	Q6H8U7	Q6h8u7 neisseria m
14	47	100.0	571	Q6H8U1	Q6h8u1 neisseria m
15	47	100.0	572	Q6H8U6	Q6h8u6 neisseria m
16	47	100.0	573	Q6H8T6	Q6h8t6 neisseria m
17	47	100.0	579	Q6H8T7	Q6h8t7 neisseria m
18	47	100.0	579	Q6H8U1	Q6h8u1 neisseria m
19	47	100.0	582	Q6PCS3	Q6fcs1 neisseria m
20	47	100.0	582	Q6PCS3	Q6fcs3 neisseria m
21	47	100.0	586	Q6H8U0	Q6h8u0 neisseria m
22	47	100.0	593	Q44169	Q44169 actinobacil
23	47	100.0	593	Q6H8V1	Q6h8v1 neisseria f
24	47	100.0	593	Q6H8W4	Q6h8w4 neisseria f
25	47	100.0	593	Q6H8W5	Q6h8w5 neisseria c
26	47	100.0	594	Q6H8W6	Q6h8w6 neisseria s
27	47	100.0	594	Q6H8V8	Q6h8v8 neisseria m
28	47	100.0	594	Q6H8W0	Q6h8w0 neisseria f
29	47	100.0	594	Q6H8W1	Q6h8w1 neisseria f
30	47	100.0	594	Q6H8W3	Q6h8w3 neisseria f
31	47	100.0	596	Q71R44	Q71r44 actinobacil
32	47	100.0	596	Q83UA7	Q83ua7 actinobacil

32	47	100.0	599	1	TBB2_NEIMB	Q05988 neisseria m
33	47	100.0	599	2	Q6H8V0	Q6h8v0 neisseria l
34	47	100.0	599	2	Q6H8V2	Q6h8v2 neisseria p
35	47	100.0	599	2	Q6H8V4	Q6h8v4 neisseria p
36	47	100.0	599	2	Q6H8V5	Q6h8v5 neisseria p
37	47	100.0	599	2	Q6H8V9	Q6h8v9 neisseria l
38	47	100.0	599	2	Q71US2	Q71us2 neisseria m
39	47	100.0	602	2	OS3991	OS3991 neisseria m
40	47	100.0	603	2	OS3992	OS3992 neisseria m
41	47	100.0	605	2	Q6H8V3	Q6h8v3 neisseria p
42	47	100.0	605	2	Q6H8V6	Q6h8v6 neisseria p
43	47	100.0	625	1	TBP2_HAEIN	P44971 haemophilus
44	47	100.0	630	2	Q48042	Q48042 haemophilus
45	47	100.0	631	2	Q48041	Q48041 haemophilus

ALIGNMENTS

RESULT 1

Q6DKQ8 PRELIMINARY; PRT; 60 AA.
AC Q6DKQ8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DS Transferrin binding protein B (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OX Neisseriaceae; Neisseria.
CX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RA Trivedi S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY680951; AAT71325.1; -
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6509 MW; 5A7424D75DFADCF4 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 1 LEGGFYGP 8
Db 52 LEGGFYGP 59
|||||||
|||||||

RESULT 2

Q6H8U3 PRELIMINARY; PRT; 410 AA.
ID Q6H8U3;
AC Q6H8U3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=cbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OX Neisseriaceae; Neisseria.
CX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha3;
RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704753; CAG28835.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.

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DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON TER 1
SQ SEQUENCE 410 AA; 45729 MW; E6CDB0771C99A15B CRC64;

Query Match 100.0%; Score 47; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 288 LEGGFYGP 295
|||||
PRT; 547 AA.

RESULT 3
Q71R42 PRELIMINARY; PRT; 526 AA.
AC Q71R42;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Haemophilus parasuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=738;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H411;
RA Ladrón N., de la Puente V., Ferri E.F.R., Navas J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF376035; AAQ02784.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
SQ SEQUENCE 526 AA; 57619 MW; A33EE197C9327EE3 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 271 LEGGFYGP 278
|||||
PRT; 545 AA.

RESULT 4
Q71R38 PRELIMINARY; PRT; 545 AA.
AC Q71R38;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B.
GN Name=tbpB;
OS Haemophilus parasuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=738;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H413;
RA de la Puente V., Ladrón N., Ferri E.F.R., Navas J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378124; AAQ02788.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
SQ SEQUENCE 545 AA; 59754 MW; EA12E851A295756D CRC64;

Query Match 100.0%; Score 47; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 271 LEGGFYGP 278
|||||
PRT; 547 AA.

RESULT 5
Q44124 PRELIMINARY; PRT; 547 AA.
AC Q44124;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin binding protein 2.
GN Name=tbpB;
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H49;
RA MEDLINE=96036198; PubMed=7582000;
RA Gonzalez G.C., Yu R.H., Rostock P.R.Jr., Schryvers A.B.;
RT "Sequence, genetic analysis, and expression of Actinobacillus
RT pleuropneumoniae transferrin receptor genes.";
RL Microbiology 141:2405-2416(1995).
DR EMBL; U16017; AAC43484.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
SQ SEQUENCE 547 AA; 59818 MW; B8A5D096FBAD088C CRC64;

Query Match 100.0%; Score 47; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 272 LEGGFYGP 279
|||||
PRT; 547 AA.

RESULT 6
Q44168 PRELIMINARY; PRT; 547 AA.
AC Q44168;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein; transferrin-binding protein.
GN Name=tfbA;
OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=biotype 2-serotype 2;
RA Bunka S., Potter A., Gerlach G.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z46775; CAA86730.1; -.
DR PIR; S49815; S49815.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
SQ SEQUENCE 547 AA; 59790 MW; F73734C5A7AC3C56 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 272 LEGGFYGP 279
|||||
PRT; 547 AA.

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Db      272 LEGGFYGP 279

RESULT 7
Q44170
ID      Q44170      PRELIMINARY;      PRT;      547 AA.
AC      Q44170;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Transferrin-binding protein.
GN      Name=tbpA;
OS      Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC      Pasteurellaceae; Actinobacillus.
OX      NCBI_TaxID=715;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=serotype 7; PubMed=1639494;
RX      MEDLINE=92347999;
RA      Gerlach G.F., Klashinsky S., Anderson C., Potter A.A., Wilson P.J.;
RT      "Characterization of two genes encoding distinct transferrin-binding
RL      proteins in different Actinobacillus pleuropneumoniae isolates.";
RT      Infect. Immun. 60:3253-3261(1992).
DR      EMBL; M85275; AA21929.1; -.
DR      FIR; A44796; A44796.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0004998; F:transferrin receptor activity; IEA.
DR      InterPro; IPR001677; Transferrin_bind.
DR      Pfam; PF01298; Lipoprotein_5; 1.
SQ      SEQUENCE 547 AA; 59849 MW; C3C870FF5867630F CRC64;

Query Match      100.0%; Score 47; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEGGFYGP 8
Db      272 LEGGFYGP 279

RESULT 8
Q71R40
ID      Q71R40      PRELIMINARY;      PRT;      560 AA.
AC      Q71R40;
DT      05-JUL-2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE      Transferrin binding protein B.
GN      Name=tbpB;
OS      Haemophilus parasuis.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC      Pasteurellaceae; Haemophilus.
OX      NCBI_TaxID=738;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=H410;
RA      Ladrón N., de la Puente V., Ferri E.F.R., Navas J.;
RL      Submitted (MAY-2001) to the EMBL/GenBank/DBSJ databases.
DR      EMBL; AP376775; AAQ20786.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0004998; F:transferrin receptor activity; IEA.
DR      InterPro; IPR001677; Transferrin_bind.
DR      Pfam; PF01298; Lipoprotein_5; 1.
SQ      SEQUENCE 560 AA; 61713 MW; 0914C717B69007DC CRC64;

Query Match      100.0%; Score 47; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEGGFYGP 8
Db      288 LEGGFYGP 295

RESULT 9
Q6H8U4
ID      Q6H8U4      PRELIMINARY;      PRT;      566 AA.
AC      Q6H8U4;
DT      05-JUL-2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE      Transferrin binding protein B (Fragment).
GN      Name=tbpB;
OS      Neisseria meningitidis.
OC      Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC      Neisseriaceae; Neisseria.
OX      NCBI_TaxID=487;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Alpha261;
RA      Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL      Submitted (MAY-2004) to the EMBL/GenBank/DBSJ databases.
DR      EMBL; AJ704752; CAG28834.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0004998; F:transferrin receptor activity; IEA.
DR      InterPro; IPR001677; Transferrin_bind.
DR      Pfam; PF01298; Lipoprotein_5; 1.
DR      NON_TER 1
FT      NON_TER 566
FT      NON_TER 567
SQ      SEQUENCE 566 AA; 61751 MW; E0FCA99B682412D8 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEGGFYGP 8
Db      291 LEGGFYGP 298

RESULT 10
Q6H8U0
ID      Q6H8U0      PRELIMINARY;      PRT;      567 AA.
AC      Q6H8U0;
DT      05-JUL-2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE      Transferrin binding protein B (Fragment).
GN      Name=tbpB;
OS      Neisseria meningitidis.
OC      Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC      Neisseriaceae; Neisseria.
OX      NCBI_TaxID=487;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Alpha563;
RA      Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL      Submitted (MAY-2004) to the EMBL/GenBank/DBSJ databases.
DR      EMBL; AJ704756; CAG28838.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0004998; F:transferrin receptor activity; IEA.
DR      InterPro; IPR001677; Transferrin_bind.
DR      Pfam; PF01298; Lipoprotein_5; 1.
DR      NON_TER 1
FT      NON_TER 567
FT      NON_TER 567
SQ      SEQUENCE 567 AA; 61960 MW; 60271A7D3F306892 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 567;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LEGGFYGP 8
Db      288 LEGGFYGP 295

RESULT 11

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Q6H8T9
ID Q6H8T9 PRELIMINARY; PRT; 569 AA.
AC Q6H8T9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha706;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704757; CAG28839.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON TER 1
FT NON TER 569
SQ SEQUENCE 569 AA; 62323 MW; F7C31612B9152DEF CRC64;

Query Match 100.0%; Score 47; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 288 LEGGFYGP 295

RESULT 12
Q6H8U2
ID Q6H8U2 PRELIMINARY; PRT; 569 AA.
AC Q6H8U2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha306, Alpha749, and Alpha223;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704754; CAG28836.1; -.
DR EMBL; AJ704758; CAG28840.1; -.
DR EMBL; AJ704751; CAG28833.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON TER 1
FT NON TER 569
SQ SEQUENCE 569 AA; 62472 MW; 6AFCB640D99DCA2F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 288 LEGGFYGP 295

Q6H8T9
ID Q6H8T9 PRELIMINARY; PRT; 569 AA.
AC Q6H8T9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha706;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704757; CAG28839.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON TER 1
FT NON TER 569
SQ SEQUENCE 569 AA; 62323 MW; F7C31612B9152DEF CRC64;

Query Match 100.0%; Score 47; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 288 LEGGFYGP 295

Q6H8U2
ID Q6H8U2 PRELIMINARY; PRT; 569 AA.
AC Q6H8U2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha306, Alpha749, and Alpha223;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704754; CAG28836.1; -.
DR EMBL; AJ704758; CAG28840.1; -.
DR EMBL; AJ704751; CAG28833.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON TER 1
FT NON TER 569
SQ SEQUENCE 569 AA; 62472 MW; 6AFCB640D99DCA2F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 288 LEGGFYGP 295

```

```

RESULT 13
Q6H8U7
ID Q6H8U7 PRELIMINARY; PRT; 570 AA.
AC Q6H8U7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha122;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704749; CAG28831.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON TER 1
FT NON TER 570
SQ SEQUENCE 570 AA; 62724 MW; 622F1F15CACH37C9 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 570;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 288 LEGGFYGP 295

RESULT 14
Q6H8U1
ID Q6H8U1 PRELIMINARY; PRT; 571 AA.
AC Q6H8U1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alpha313;
RA Harrison O.B., Claus H., Vogel U., Bennett J., Maiden M., Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704755; CAG28837.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON TER 1
FT NON TER 571
SQ SEQUENCE 571 AA; 62265 MW; E3FDEB33921EC2D4 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYGP 8
Db 292 LEGGFYGP 299

RESULT 15

```

Q6H8U6
ID Q6H8U6 PRELIMINARY; PRT; 572 AA.
AC Q6H8U6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Transferrin binding protein B (Fragment).
GN Name=tbpB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Alphal7;
RA Harrison O.B.; Claus H.; Vogel U.; Bennett J.; Maiden M.; Rokbi B.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ704750; CAG28832.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004998; F:transferrin receptor activity; IEA.
DR InterPro; IPR001677; Transferrin_bind.
DR Pfam; PF01298; Lipoprotein_5; 1.
FT NON_TER 1
FT NON_TER 572
SQ SEQUENCE 572 AA; 62540 MW; 049BFPAD043ACBD0A CRC64;
Query Match 100.0%; Score 47; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LEGFPYGP 8
Db 292 LEGFPYGP 299

Search completed: November 9, 2005, 19:16:35
Job time : 33.4938 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 9, 2005, 18:43:14 ; Search time 31.6296 Seconds
(without alignments)
85.595 Million cell updates/sec

Title: US-10-043-344-85

Perfect score: 40

Sequence: 1 LEGGPG 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	7	2 AAR77969	Aar77969 Antigenic
2	40	100.0	7	2 AAW46162	Aaw46162 Predicted
3	40	100.0	7	2 AAY51767	Aay51767 H. influe
4	40	100.0	7	2 AAW54121	Aaw54121 Tbp2 anti
5	40	100.0	7	2 AAW89426	Aaw89426 Moraxella
6	40	100.0	7	3 AAY80464	Aay80464 H. influe
7	40	100.0	8	2 AAR77958	Aar77958 Antigenic
8	40	100.0	8	2 AAW46151	Aaw46151 Predicted
9	40	100.0	8	2 AAY51756	Aay51756 H. influe
10	40	100.0	8	2 AAW54110	Aaw54110 Tbp2 anti
11	40	100.0	8	3 AAY80453	Aay80453 H. influe
12	40	100.0	15	2 AAR77974	Aar77974 H. influe
13	40	100.0	15	2 AAY51789	Aay51789 H. influe
14	40	100.0	15	2 AAW54133	Aaw54133 Polioviru
15	40	100.0	15	3 AAY80391	Aay80391 H. influe
16	40	100.0	16	2 AAR77973	Aar77973 H. influe
17	40	100.0	16	2 AAY51787	Aay51787 H. influe
18	40	100.0	16	2 AAY51788	Aay51788 H. influe
19	40	100.0	16	2 AAW54132	Aaw54132 Polioviru
20	40	100.0	16	2 AAW54131	Aaw54131 Polioviru
21	40	100.0	16	3 AAY80390	Aay80390 H. influe
22	40	100.0	16	3 AAY80389	Aay80389 H. influe
23	40	100.0	17	2 AAR77971	Aar77971 H. influe
24	40	100.0	17	2 AAY51786	Aay51786 H. influe
25	40	100.0	17	2 AAW54130	Aaw54130 Polioviru

ALIGNMENTS

RESULT 1

AAR77969
ID AAR77969 standard; peptide; 7 AA.

XX

AC AAR77969;

XX 09-OCT-1996 (first entry)

DT Antigenic Tbp2 peptide TBP2-36.

DE Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen;

KW non-typable strain; Haemophilus influenzae; meningitis.

KW Synthetic.

OS WO9513370-A1.

PN 18-MAY-1995.

XX 07-NOV-1994; 94WO-CA000616.

XX 08-NOV-1993; 93US-00148968.

XX 29-DEC-1993; 93US-00175116.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;

XX Yang Y, Murdin A, Klein M;

XX WPI; 1995-194089/25.

XX Nucleic acids encoding Haemophilus transferrin receptor - used to develop

XX prods for detection and in diagnosis, prevention and treatment of

XX Haemophilus infection.

XX Claim 11; Page 73; 231pp; English.

XX AAR77933-969 are predicted antigenic peptides derived from conserved

XX regions of the Tbp2 protein from H. influenzae strains Egan, Minna, D163

XX and non-typable strain PAK12085. The transferrin receptor (TfR) operon

XX consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are

XX transcribed from a single promoter. H. influenzae TfR is iron- and/or

XX haemin-regulated and a putative fur-binding site has been identified

XX upstream of tbp2. Antibodies blocking this binding site may prevent

XX bacterial growth. Fragments of the TfR (for its genes) are useful in

XX vaccines to provide protection against, e.g. bacterial meningitis. An

XX advantage of using the TfR is that it shares homology with TfR of other

XX H. influenzae strains including non-typable strains. According to the

Aay80388 H. influe
Aar77934 Antigenic
Aaw46127 Predicted
Aay51732 H. influe
Aaw53087 Tbp2 anti
Aay80429 H. influe
Aar77945 Antigenic
Aaw46138 Predicted
Aay51743 H. influe
Aaw53098 Tbp2 anti
Aay80440 H. influe
Aay29819 Bacterici
Aaw43004 Truncated
Aay51809 H. influe
Aaw00504 N.meningi
Aar98887 N.meningi
Aaw14644 N. mening
Aaw43005 Truncated
Aay51808 H. influe
Aaw43006 Truncated

26 40 100.0 17 3 AAY80388
27 40 100.0 31 2 AAR77934
28 40 100.0 31 2 AAW46127
29 40 100.0 31 2 AAY51732
30 40 100.0 31 2 AAW53087
31 40 100.0 31 3 AAY80429
32 40 100.0 35 2 AAR77945
33 40 100.0 35 2 AAW46138
34 40 100.0 35 2 AAY51743
35 40 100.0 35 2 AAW53098
36 40 100.0 35 3 AAY80440
37 40 100.0 38 2 AAY29819
38 40 100.0 310 2 AAW43004
39 40 100.0 310 2 AAY51809
40 40 100.0 325 2 AAW00504
41 40 100.0 340 2 AAR98887
42 40 100.0 340 2 AAW14644
43 40 100.0 365 2 AAW43005
44 40 100.0 365 2 AAY51808
45 40 100.0 404 2 AAW43006

CC specification the present sequence shows residues 231-238 of Tbp2 from
 CC the H. influenzae strain Egan
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7
 |||||
 Db 1 LEGGFYG 7

RESULT 2
 AAW46162
 ID AAW46162 standard; protein; 7 AA.

XX AC AAW46162;

XX 05-MAY-1998 (first entry)

DE Predicted antigenic Tbp1 peptide TBP2-36.

XX Transferrin receptor; Haemophilus influenzae type b; iron;
 KW human transferrin; iron source; antibody; bacterial growth; vaccine;
 KW immunogenic truncated analogue; antigen; Tbp1; Tbp2.

XX Synthetic.
 OS Haemophilus influenzae.

XX WO9640929-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-CA000399.

XX 07-JUN-1995; 95US-00483577.

XX 17-MAY-1996; 96US-00649518.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loosmore SM, Harkness RE, Schryvers AB, Chong P, Gray-Owen S;
 PI Yang Y, Mordin AD, Klein MH;

XX WPI; 1997-052329/05.

XX Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used
 PT to induce protection against disease caused by transferrin producing
 PT pathogens, or as antigen to detect Haemophilus Tfr antibodies.

PS Example 16; Page 71; 228pp; English.

XX AAW46162-62 are predicted antigenic peptides derived from the Tbp2
 CC protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin
 CC receptor, of which Tbp1 is also a subunit. The deduced amino acid
 CC sequences of Tbp1 and Tbp2 were compared, and regions of conservation
 CC identified. The above peptides are derived from these regions, the
 CC present peptide being derived from residues 231-238. Iron is an essential
 CC nutrient for the growth of these bacteria, and they can utilise human
 CC transferrin as a source of iron. Antibodies which block the access of the
 CC transferrin receptor to its iron source prevent bacterial growth. The
 CC transferrin receptor, or fragments, therefore, are good vaccine
 CC candidates. An immunogenic composition comprising (or encoding) the
 CC immunogenic truncated analogue can be used to induce protection against a
 CC disease caused by a bacterial pathogen that produces the transferrin
 CC receptor. The immunogenic truncated analogue is also useful as an antigen
 CC in immunoassays for the detection of Haemophilus transferrin receptor
 CC antibodies, while the nucleic acid molecule can be used as a
 CC hybridisation probe for the detection of other transferrin receptor genes

XX Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7
 |||||
 Db 1 LEGGFYG 7

RESULT 3

AA51767
 ID AA51767 standard; protein; 7 AA.

XX AC AA51767;

XX 13-JUN-2000 (first entry)

DE H. influenzae antigenic Tbp2 peptide TBP2-36.

XX Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
 KW diagnosis.

XX Haemophilus influenzae.

XX US6015688-A.

XX 18-JAN-2000.

XX 07-JUN-1995; 95US-00483577.

XX 08-NOV-1993; 93US-00148968.

XX 29-DEC-1993; 93US-00175116.

XX 08-NOV-1994; 94US-00337483.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
 PI Mordin A, Klein M, Chong P;

XX WPI; 1997-052329/05.

XX Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used
 PT to induce protection against disease caused by transferrin producing
 PT pathogens, or as antigen to detect Haemophilus Tfr antibodies.

PS Example 16; Col 39-40; 281pp; English.

XX This invention describes a novel isolated and purified nucleic acid (I)
 CC encoding an immunogenic, C-terminally truncated analog of one of the
 CC transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae
 CC which has antibacterial activity. (I) are used for recombinant production
 CC of truncated Tbp; as probes and primers for detecting, and diagnosing
 CC infection by, Haemophilus, also for isolating similar sequences from
 CC other bacteria; as immunogens for vaccinating against infections caused
 CC by bacteria that produce transferrin receptors, e.g. Haemophilus,
 CC Neisseria or Branhamella. The truncated proteins are useful as immunogens
 CC (as above); for diagnosing infection (as antigens in immunoassays) and
 CC for raising antibodies, used for diagnosis of infections or for passive
 CC immunization. AA51695-Y51767 represent H. influenzae transferrin
 CC receptor proteins Tbp1 and Tbp2 antigenic peptide fragments

SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7
 |||||
 Db 1 LEGGFYG 7

RESULT 4

```

AAW54121
ID AAW54121 standard; peptide; 7 AA.
XX
XX AC AAW54121;
XX
XX DT 20-JUN-1998 (first entry)
XX
XX DE Tbp2 antigenic peptide TBP2-36.
XX
XX KW tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis;
XX KW passive immunisation; transferrin receptor operon.
XX OS Haemophilus influenzae.
XX
XX PN US5708149-A.
XX
XX PD 13-JAN-1998.
XX
XX PF 07-JUN-1995; 95US-00487890.
XX
XX PR 08-NOV-1993; 93US-00148968.
XX PR 29-DEC-1993; 93US-00175116.
XX PR 08-NOV-1994; 94US-00337483.
XX
XX PA (CONN-) CONNAUGHT LAB LTD.
XX
XX PI Gray-Owen S, Klein M, Harkness R, Loosmore S, Yang Y, Chong P;
XX PI Murdin A, Schryvers A;
XX
XX DR WPI; 1998-100410/09.
XX
XX PT Purification of recombinant Haemophilus transferrin-binding protein - by
XX PT solubilising inclusion bodies separated from cell lysate.
XX
XX PS Example 16/17; Column 37-38; 261pp; English.
XX
XX CC Peptides AAW53086-W53100 and peptides AAW54100-W54122 are derived from
XX CC the Tbp2 protein. The Tbp2 protein is one of two proteins with genes
XX CC found on the transferrin operon. These peptides can be used along with
XX CC the genes, DNA sequences and recombinant proteins for diagnosis,
XX CC immunisation and the generation of diagnostic and immunological reagents.
XX CC They can also be used to protect from bacteria that produce transferrin
XX CC receptor protein
XX
XX SQ Sequence 7 AA;
XX
XX Query Match 100.0%; Score 40; DB 2; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LEGGFGY 7
XX |||||
XX Db 1 LEGGFGY 7
XX
XX RESULT 5
XX AAW89426
XX ID AAW89426 standard; peptide; 7 AA.
XX
XX AC AAW89426;
XX
XX DT 21-JUN-1999 (first entry)
XX
XX DE Moraxella lactoferrin binding protein 2 (Lbp2) epitope.
XX
XX KW Lactoferrin receptor; lactoferrin binding protein; Lbp1; lbpA gene;
XX KW infection; otitis media; sinusitis; conjunctivitis; pneumonia;
XX KW bronchitis; tracheitis; emphysema; diagnosis; therapy; vaccine;
XX KW Branhamella catarrhalis; epitope.
XX
XX OS Moraxella catarrhalis.
XX
XX PN W09855606-A2.
XX
XX Query Match 100.0%; Score 40; DB 2; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LEGGFGY 7
XX |||||
XX Db 1 LEGGFGY 7
XX
XX RESULT 6
XX AAY80464
XX ID AAY80464 standard; peptide; 7 AA.
XX
XX AC AAY80464;
XX
XX DT 06-JUN-2000 (first entry)
XX
XX DE H. influenzae transferrin receptor Tbp1 epitope TBP2-36.
XX
XX KW Antibacterial; antiinflammatory; auditory; respiratory; antibody;
XX KW antiserum; transferrin receptor; immunogen; epitope; otitis media;
XX KW bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.
XX
XX OS Haemophilus influenzae.
XX
XX PN US6008326-A.
XX
XX PD 28-DEC-1999.
XX
XX PF 07-JUN-1995; 95US-00474671.
XX
XX PR 08-NOV-1993; 93US-00148968.
XX PR 29-DEC-1993; 93US-00175116.
XX PR 08-NOV-1995; 95US-00337483.
XX
XX PA (CONN-) CONNAUGHT LAB LTD.
XX
XX PI Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;
XX PI Murdin A, Schryvers A;
XX
XX DR WPI; 2000-096387/08.
XX
XX PT Antibodies specific for transferrin receptor proteins of Haemophilus

```

PT influenzae, useful for treating otitis media, epiglottitis, pneumonia and
 XX tracheobronchitis.

PS Disclosure; Col 39-40; 252pp; English.

XX The invention relates to novel antibodies (or monospecific antisera)
 CC specific for single transferrin receptor proteins (or immunogenic
 CC fragment) from strains of Haemophilus influenzae. This sequence
 CC corresponds to an epitope from the H. influenzae transferrin receptor
 CC protein Tbp2. The antibodies may be used for preventing and treating
 CC infections and disorders caused by H. influenzae, including bacterial
 CC meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis.
 CC The antibodies may also be used to detect the presence of H. influenzae
 CC proteins in samples according to standard methodologies (e.g. enzyme
 CC linked immunosorbent assay (ELISA)) and hence diagnose infections
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7
 Db 1 LEGGFYG 7

RESULT 7

AAR77958
 ID AAR77958 standard; peptide; 8 AA.

XX AAR77958;

DT 09-OCT-1996 (first entry)

XX Antigenic Tbp2 peptide TBP2-25.

XX Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen;
 KW non-typable strain; Haemophilus influenzae; meningitis.

XX Synthetic.

XX WO9513370-A1.

XX 18-MAY-1995.

XX 07-NOV-1994; 94WO-CA000616.

XX 08-NOV-1993; 93US-00148968.

XX 29-DEC-1993; 93US-00175116.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loomore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;
 PI Yang Y, Murdin A, Klein M;

XX WPI; 1995-194089/25.

XX Nucleic acids encoding Haemophilus transferrin receptor - used to develop
 PT prods for detection and in diagnosis, prevention and treatment of
 PT Haemophilus infection.

XX Claim 11; Page 72; 231pp; English.

XX AAR77933-969 are predicted antigenic peptides derived from conserved
 CC regions of the Tbp2 protein from H. influenzae strains Egan, Minna, DL63
 CC and non-typable strain PAK12085. The transferrin receptor (TfR) operon
 CC consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are
 CC transcribed from a single promoter. H. influenzae TfR is iron- and/or
 CC haemin-regulated and a putative fur-binding site has been identified
 CC upstream of Tbp2. Antibodies blocking this binding site may prevent
 CC bacterial growth. Fragments of the TfR (or its genes) are useful in
 CC vaccines to provide protection against, e.g. bacterial meningitis. An

CC advantage of using the TfR is that it shares homology with TfR of other
 CC H. influenzae strains including non-typable strains. According to the
 CC specification the present sequence shows residues 231-238 of Tbp2 from
 CC the H. influenzae strain Egan

XX Sequence 8 AA;

Query Match 100.0%; Score 40; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LEGGFYG 7
 Db 1 LEGGFYG 7

RESULT 8

AAW46151

ID AAW46151 standard; protein; 8 AA.

XX AAW46151;

XX 05-MAY-1998 (first entry)

XX Predicted antigenic Tbp1 peptide TBP2-25.

XX Transferrin receptor; Haemophilus influenzae type b; iron;
 KW human transferrin; iron source; antibody; bacterial growth; vaccine;
 KW immunogenic truncated analogue; antigen; Tbp1; Tbp2.

XX Synthetic.

XX Haemophilus influenzae.

XX WO9640929-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-CA000399.

XX 07-JUN-1995; 95US-00483577.

XX 17-MAY-1996; 96US-00649518.

XX (CONN-) CONNAUGHT LAB LTD.

XX Loomore SM, Harkness RE, Schryvers AB, Chong P, Gray-Owen S;
 PI Yang Y, Murdin AD, Klein MH;

XX WPI; 1997-052329/05.

XX Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used
 PT to induce protection against disease caused by transferrin producing
 PT pathogens, or as antigen to detect Haemophilus TfR antibodies.

XX Example 16; Page 71; 228pp; English.

XX AAW46126-62 are predicted antigenic peptides derived from the Tbp2
 CC protein of Haemophilus influenzae type b. Tbp2 is part of the transferrin
 CC receptor, of which Tbp1 is also a subunit. The deduced amino acid
 CC sequences of Tbp1 and Tbp2 were compared, and regions of conservation
 CC identified. The above peptides are derived from these regions, the
 CC present peptide being derived from residues 231-238. Iron is an essential
 CC nutrient for the growth of these bacteria, and they can utilise human
 CC transferrin as a source of iron. Antibodies which block the access of the
 CC transferrin receptor to its iron source prevent bacterial growth. The
 CC transferrin receptor, or fragments, therefore, are good vaccine
 CC candidates. An immunogenic composition comprising (or encoding) the
 CC immunogenic truncated analogue can be used to induce protection against a
 CC disease caused by a bacterial pathogen that produces the transferrin
 CC receptor. The immunogenic truncated analogue is also useful as an antigen
 CC in immunoassays for the detection of Haemophilus transferrin receptor
 CC antibodies, while the nucleic acid molecule can be used as a
 CC hybridisation probe for the detection of other transferrin receptor genes
 XX

```

SQ      Sequence 8 AA;
Query Match      100.0%; Score 40; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEGGPGY 7
Db      1 LEGGPGY 7

RESULT 9
AAW51756
ID      AAW51756 standard; protein; 8 AA.
XX
AC      AAW51756;
XX
DT      13-JUN-2000 (first entry)
XX
DE      H. influenzae antigenic Tbp2 peptide TBP2-25.
XX
KW      Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
KW      diagnosis.
XX
OS      Haemophilus influenzae.
XX
PN      US6015688-A.
XX
PD      18-JAN-2000.
XX
PF      07-JUN-1995; 95US-00483577.
XX
PR      08-NOV-1993; 93US-00148968.
PR      29-DEC-1993; 93US-00175116.
PR      08-NOV-1994; 94US-00337483.
XX
PA      (CONN-) CONNAUGHT LAB LTD.
XX
PI      Loosmore S., Harkness R., Schryvers A., Gray-Owen S., Yang Y;
PI      Murdin A., Klein M., Chong P;
XX
WPI; 1997-052329/05.
XX
Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used
PT to induce protection against disease caused by transferrin producing
PT pathogens, or as antigen to detect Haemophilus Tfr antibodies.
XX
Example 16; Col 39-40; 281pp; English.
XX
This invention describes a novel isolated and purified nucleic acid (I)
CC encoding an immunogenic, C-terminally truncated analog of one of the
CC transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae
CC which has antibacterial activity. (I) are used for recombinant production
CC of truncated Tbp; as probes and primers for detecting, and diagnosing
CC infection by, Haemophilus, also for isolating similar sequences from
CC other bacteria; as immunogens for vaccinating against infections caused
CC by bacteria that produce transferrin receptors, e.g. Haemophilus,
CC Neisseria or Branhamella. The truncated proteins are useful as immunogens
CC (as above); for diagnosing infection (as antigens in immunoassays) and
CC for raising antibodies, used for diagnosis of infections or for passive
CC immunization. AAY51695-Y51767 represent H. influenzae transferrin
CC receptor proteins Tbp1 and Tbp2 antigenic peptide fragments
XX
Sequence 8 AA;
Query Match      100.0%; Score 40; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEGGPGY 7
Db      1 LEGGPGY 7

RESULT 10
AAW54110
ID      AAW54110 standard; peptide; 8 AA.
XX
AC      AAW54110;
XX
DT      20-JUL-1998 (first entry)
XX
DE      Tbp2 antigenic peptide TBP2-25.
XX
KW      tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis;
KW      passive immunisation; transferrin receptor operon.
XX
OS      Haemophilus influenzae.
XX
PN      US5708149-A.
XX
PD      13-JAN-1998.
XX
PF      07-JUN-1995; 95US-00487890.
XX
PR      08-NOV-1993; 93US-00148968.
PR      29-DEC-1993; 93US-00175116.
PR      08-NOV-1994; 94US-00337483.
XX
PA      (CONN-) CONNAUGHT LAB LTD.
XX
PI      Gray-Owen S., Klein M., Harkness R., Loosmore S., Yang Y, Chong P;
PI      Murdin A., Schryvers A;
XX
WPI; 1998-100410/09.
XX
Purification of recombinant Haemophilus transferrin-binding protein - by
PT solubilising inclusion bodies separated from cell lysate.
XX
Example 16/17; Column 37-38; 261pp; English.
XX
Peptides AAW53086-W53100 and peptides AAW54100-W54122 are derived from
CC the Tbp2 protein. The Tbp2 protein is one of two proteins with genes
CC found on the transferrin operon. These peptides can be used along with
CC the genes, DNA sequences and recombinant proteins for diagnosis.
CC immunisation and the generation of diagnostic and immunological reagents.
CC They can also be used to protect from bacteria that produce transferrin
CC receptor protein
XX
Sequence 8 AA;
Query Match      100.0%; Score 40; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LEGGPGY 7
Db      1 LEGGPGY 7

RESULT 11
AAY80453
ID      AAY80453 standard; peptide; 8 AA.
XX
AC      AAY80453;
XX
DT      06-JUN-2000 (first entry)
XX
DE      H. influenzae transferrin receptor Tbp1 epitope TBP2-25.
XX
KW      Antibacterial; antinflammatory; auditory; respiratory; antibody;
KW      antiserum; transferrin receptor; immunogen; epitope; otitis media;
KW      bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.
XX
OS      Haemophilus influenzae.
XX

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PN US6008326-A.
XX
XX 28-DEC-1999.
XX
XX 07-JUN-1995; 95US-00474671.
XX
XX 08-NOV-1993; 93US-00148968.
XX
XX 29-DEC-1993; 93US-00175116.
XX
XX 08-NOV-1995; 95US-00337483.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;
XX Murdin A, Schryvers A;
XX
XX WPI; 2000-096387/08.
XX
XX Antibodies specific for transferrin receptor proteins of Haemophilus
XX influenzae, useful for treating otitis media, epiglottitis, pneumonia and
XX tracheobronchitis.
XX
XX Disclosure; Col 37-38; 252pp; English.
XX
XX The invention relates to novel antibodies (or monospecific antisera)
XX specific for single transferrin receptor proteins (or immunogenic
XX fragment) from strains of Haemophilus influenzae. This sequence
XX corresponds to an epitope from the H. influenzae transferrin receptor
XX protein Tbp2. The antibodies may be used for preventing and treating
XX infections and disorders caused by H. influenzae, including bacterial
XX meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis.
XX The antibodies may also be used to detect the presence of H. influenzae
XX proteins in samples according to standard methodologies (e.g. enzyme
XX linked immunosorbent assay (ELISA)) and hence diagnose infections
XX
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 40; DB 3; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LEGGFYG 7
XX |||||
XX 1 LEGGFYG 7
XX
XX
XX RESULT 12
XX AAR77974
XX ID AAR77974 standard; peptide; 15 AA.
XX
XX AC AAR77974;
XX
XX DT 09-OCT-1996 (first entry)
XX
XX DE H. influenzae TBP2 epitope used to construct pT7TBP2D.
XX
XX KW Tbp1; Tbp2; transferrin receptor operon; vaccine; antigen; vector;
XX non-typable strain; Haemophilus influenzae; meningitis; poliovirus.
XX
XX OS Synthetic.
XX
XX PN W09513370-A1.
XX
XX PD 18-MAY-1995.
XX
XX PF 07-NOV-1994; 94WO-CA000616.
XX
XX PR 08-NOV-1993; 93US-00148968.
XX
XX PR 29-DEC-1993; 93US-00175116.
XX
XX PA (CONN-) CONNAUGHT LAB LTD.
XX
XX Loosmore S, Harkness R, Schryvers A, Chong P, Gray-Owen S;
XX Yang Y, Murdin A, Klein M;
XX
XX
XX
XX WPI; 1995-194089/25.
XX
XX Nucleic acids encoding Haemophilus transferrin receptor - used to develop
XX prods for detection and in diagnosis, prevention and treatment of
XX Haemophilus infection.
XX
XX Example 20; Fig 29; 231pp; English.
XX
XX The transferrin receptor (TfR) operon consists of two genes (Tbp1 and
XX Tbp2) arranged in tandem and which are transcribed from a single
XX promoter. Fragments of the TfR (or its genes) are useful in vaccines to
XX provide protection against, e.g. bacterial meningitis. A cDNA clone
XX (AAQ94452) of the poliovirus type 1, Mahoney strain (PVI-M) genome was
XX cut with SauI and HindIII excising a fragment contg. bases 2754-2786,
XX which encodes AAR77970. (Residues 1095 is amino acid 95 of capsid protein
XX VP1). New hybrid cDNA clones encoding both poliovirus and transferrin
XX receptor amino acid sequences were constructed by replacing the excised
XX fragment with oligonucleotides encoding amino acids from H. influenzae
XX Tbp2 (AAR77971-74). Transfection of Vero cells with the hybrid RNA
XX transcripts produced 4 viable hybrid viruses, designated PVI7BP2A,
XX PVI7BP2B, PVI7BP2C and PVI7BP2D
XX
XX Sequence 15 AA;
XX
XX Query Match 100.0%; Score 40; DB 2; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 LEGGFYG 7
XX |||||
XX 7 LEGGFYG 13
XX
XX
XX RESULT 13
XX AAY51789
XX ID AAY51789 standard; protein; 15 AA.
XX
XX AC AAY51789;
XX
XX DT 13-JUN-2000 (first entry)
XX
XX DE H. influenzae transferrin receptor protein fragment #5.
XX
XX KW Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
XX diagnosis.
XX
XX OS Haemophilus influenzae.
XX
XX PN US6015688-A.
XX
XX PD 18-JAN-2000.
XX
XX PF 07-JUN-1995; 95US-00483577.
XX
XX PR 08-NOV-1993; 93US-00148968.
XX
XX PR 29-DEC-1993; 93US-00175116.
XX
XX PR 08-NOV-1994; 94US-00337483.
XX
XX PA (CONN-) CONNAUGHT LAB LTD.
XX
XX PI Loosmore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
XX PI Murdin A, Klein M, Chong P;
XX
XX DR WPI; 1997-052329/05.
XX
XX Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used
XX to induce protection against disease caused by transferrin producing
XX pathogens, or as antigen to detect Haemophilus TfR antibodies.
XX
XX Disclosure; Col 235-236; 281pp; English.
XX
XX This invention describes a novel isolated and purified nucleic acid (I)

```

CC encoding an immunogenic, C-terminally truncated analog of one of the
 CC transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae
 CC which has antibacterial activity. (1) are used for recombinant production
 CC of truncated Tbp; as probes and primers for detecting, and diagnosing
 CC infection by, Haemophilus, also for isolating similar sequences from
 CC other bacteria; as immunogens for vaccinating against infections caused
 CC by bacteria that produce transferrin receptors, e.g. Haemophilus,
 CC Neisseria or Branhamella. The truncated proteins are useful as immunogens
 CC (as above); for diagnosing infection (as antigens in immunoassays) and
 CC for raising antibodies, used for diagnosis of infections or for passive
 CC immunization. This sequence represents a fragment of a H. influenzae
 CC transferrin receptor protein
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 40; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEGGFGY 7
 |||||
 Db 7 LEGGFGY 13

RESULT 14
 AAW54133
 ID AAW54133 standard; peptide; 15 AA.
 XX
 AC AAW54133;

XX DT 20-JUL-1998 (first entry)
 XX
 XX DE Poliovirus plasmid PV1TBP2D encoded peptide.

XX DE Transferrin receptor; antigen; virus; prevention; pathogens.
 XX OS Synthetic.
 OS Poliovirus.
 OS Haemophilus influenzae.

XX PN US5708149-A.
 XX
 XX PD 13-JAN-1998.

XX PF 07-JUN-1995; 95US-00487890.
 XX
 XX PR 08-NOV-1993; 93US-00148968.
 PR 29-DEC-1993; 93US-00175116.

XX PR 08-NOV-1994; 94US-00337483.
 XX
 XX PA (CONN-) CONNAUGHT LAB LTD.

XX PI Gray-Owen S, Klein M, Harkness R, Loosmore S, Yang Y, Chong P;
 PI Murdin A, Schryvers A;
 XX
 XX WPI; 1998-100410/09.
 XX
 XX PT Purification of recombinant Haemophilus transferrin-binding protein - by
 PT solubilising inclusion bodies separated from cell lysate.
 XX
 XX PS Example 20; Fig 29; 261pp; English.

XX CC Peptides (AAW54129-W54133) are encoded by plasmids encoding a chimeric
 CC poliovirus expressing an epitope LEGGFGY. The epitope is derived from
 CC the transferrin receptor protein that is conserved among bacteria that
 CC produce transferrin receptor protein. These viruses expressed the epitope
 CC sequence in an antigenically recognisable form. Viruses based upon
 CC expressed recombinant transferrin receptor protein can be used for the
 CC prevention of diseases caused by bacterial pathogens that produce
 CC transferrin receptor
 XX
 SQ Sequence 15 AA;

QY 1 LEGGFGY 7
 |||||
 Db 7 LEGGFGY 13

Query Match 100.0%; Score 40; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEGGFGY 7
 |||||
 Db 7 LEGGFGY 13

RESULT 15
 AAY80391
 ID AAY80391 standard; protein; 15 AA.
 XX
 AC AAY80391;

XX DT 06-JUN-2000 (first entry)
 XX
 XX DE H. influenzae transferrin receptor protein epitope TBP2D.

XX KW Antibacterial; antiinflammatory; auditory; respiratory; antibody; primer;
 KW antiserum; transferrin receptor; immunogen; epitope; otitis media; PCR;
 KW bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis; ss.
 XX
 OS Haemophilus influenzae.

XX PN US6008326-A.
 XX
 XX PD 28-DEC-1999.

XX PF 07-JUN-1995; 95US-00474671.
 XX
 XX PR 08-NOV-1993; 93US-00148968.
 PR 29-DEC-1993; 93US-00175116.

XX PR 08-NOV-1995; 95US-00337483.
 XX
 XX PA (CONN-) CONNAUGHT LAB LTD.

XX PI Loosmore S, Harkness R, Chong P, Gray-Owen S, Yang Y, Klein M;
 PI Murdin A, Schryvers A;
 XX
 XX WPI; 2000-096387/08.

XX PT Antibodies specific for transferrin receptor proteins of Haemophilus
 PT influenzae, useful for treating otitis media, epiglottitis, pneumonia and
 PT tracheobronchitis.
 XX
 XX PS Example 20; Fig 29; 252pp; English.

XX CC The invention relates to novel antibodies (or monospecific antisera)
 CC specific for single transferrin receptor proteins (or immunogenic
 CC fragment) from strains of Haemophilus influenzae. The antibodies can be
 CC generated by expressing transferrin receptor epitope on the surface of a
 CC vector protein. In an example, the vector is poliovirus and the epitopes
 CC are inserted into the capsid protein VP1. This sequence corresponds to
 CC the transferrin receptor epitope TBP2D which is used to replace amino
 CC acids 95-102 of the poliovirus VP1 capsid protein (AAY80387). The
 CC antibodies may be used for preventing and treating infections and
 CC disorders caused by H. influenzae, including bacterial meningitis, otitis
 CC media, epiglottitis, pneumonia and tracheobronchitis. The antibodies may
 CC also be used to detect the presence of H. influenzae proteins in samples
 CC according to standard methodologies (e.g. enzyme linked immunosorbent
 CC assay (ELISA)) and hence diagnose infections
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 40; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEGGFGY 7
 |||||
 Db 7 LEGGFGY 13

Search completed: November 9, 2005, 19:22:43
Job time : 32.6296 secs
